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Scientific and Technical Information Center

SEARCH REQUEST FORM

51	EARCH REQUES.	I FURIVI	•
Date: Requester's Full N	ame:	Examiner # :	
Date: Requester's Full N Art Unit Phone (30 Results Format Preferred (circle): PAP		ial Number:	
*************		**********	********
To ensure an efficient and quality search, pleas	se attach a copy of the cover shee	t, claims, and abstract or fill out	the following:
Title of Invention:			
Inventors (please provide full names):			
Earliest Priority Date:			
Search Topic: Please provide a detailed statement of the search elected species or structures, keywords, synonym Define any terms that may have a special meant	is, acronynis, and registry numbe.	rs, and combine with the concept	be searched. Include the or utility of the invention.
For Sequence Searches Only Please include of the appropriate serial number.	all pertinent information (parent,	grandchild, div <u>i</u> sional, or issued p	atent numbers) along with
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	Type of Search	Vendors and Cost	
Scarcher: Bevery C 9994	NA Sequence (#)	STN	Dialog
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Date Searcher Picked Up:	Bibliographic	WWW/Internet	
Date Completed: 02-18-00	Litigation	In-house sequence	z systems (list)
Sourcher Prep & Review Time	Fulltext	Other (specify	, MP



3

***** (ME)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. Fri Feb 18 11:55:43 2000; MasPar time 16.71 Seconds 524.338 Million cell updates/sec

Description: Perfect Score: >US-08-755-584-2 (1-412) from 5858711.pep

Sequence: 2858
1 MAEPLRGRGPRSRGGRGARR......GKELPADLGLESGDLIEVWG

Scoring table: рам 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Listing Match 0% 45 summaries

Database: a-geneseq35

i:partí 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part22 23:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Statistics: Mean 35.338; Variance 185.169; scale 0.191

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	BB	ID	Description	Pred. No.
ш	2858	100.0	412	28	W34091	Mouse NF-AT interacti	2.68e-219
2	151	ω	101	32	W60079	Homo sapiens sentrin-	3.49e-02
ω	152	υ	126	38	W87497	Human SMT3-like prote	2.99e-02
4	149	5.2	102	37	W74776	Human secreted protei	4.74e-02
S	122	4.3	265	ß	W79128	FLGA insert stabilisi	2.74e+00
Q	113	4.0	673	21	W09430	Human FRX2 polypeptid	1.01e+01
7	109	3.8	1184	14	R78519	Cardiac adenylyl cycl	1.77e+01
œ	109	3.8	1184	σ	R32882	Cardiac adenylyl cycl	1.77e+01
9	106	3.7	122	<u>ω</u>	W68479	HIV-1 strain YBF30 re	2.70e+01
10	107	3.7	3248	18	R99795	Kinetochore protein C	2.35e+01
11	103	з б	228	13	R72381	S. lavendulae ORF3 ge	4.11e+01
12	102	3.6	788	25	W05393	Mouse SH3P12 protein.	4.71e+01
13	102	3.6	2205	15	R79048	Infectious rubella vi	4.71e+01
14	99	з 5	213	24	W14567	Streptococcus pneumon	7.12e+01
15	100	3.5	386	22	W18664	Fragmented human NF-H	6.21e+01
16	99	ω .5	397	20	W09048	Plasmid pHBV DN AA en	7.12e+01

4 4 5 4	3	42	41	40	39	38	37	36	<u>ω</u>	34	္အ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
9 4 4 4	95	94	95	95	97	96	96	96	97	98	96	96	96	96	96	98	98	98	97	97	97	97	98	100	99	99	99	
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5 3	34	13	39	30	23	13	35	N	34	36	36	37	17	31	ω	37	S	25	30	7	10	3	23	ري.	24	34	12	
W19919 R27205	W64483	R73918	W95400	W55819	W22017	R71498	W75999	P70768	W68095	W72145	W79083	W76827	R88587	W56325	W59829	W81665	W64302	W32362	W47525	R35450	R51053	R74990	W16376	R27745	W26327	W60667	R66452	
Human Ksr-1 (kinase s Human nestin.	Human DR4 protein.	CD protein of Branham	losis	õ	Utrophin.	tyros	cellular prote	virus g	s reinha	St	death	protein.	EBV nuclear antigen p	Amino acid sequence o	a-B-	₽~		⋚		Human eps8.	Barr r	arr v	pept	ᠬ	1a-1	E.coli cold shock pro	Serine-rich AF-9 prot	
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Best Local :
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14-MAY-1998.
05-NOV-1996; US-030302.
(TEXA) UNIV TEXAS SYSTE
cell death in tumours
Claim 4; Page 78; 130pp; English.
Claim 4; Page 78; 130pp; English.
The sequence is that of the sentrin-1 polypeptide.
Sentrin polypeptides have the ability to protect or guard cells from tumour necrosis factor (TNF) or Fas/APO induced cell death (apoptosis). Inhibitors of the sentrin polypeptides, e.g. antibodies, can be used for inducing cell death, particularly in tumours. The products can also be used for determining the aggressiveness of a tumour and for detection and isolation of products. The sentrin polypeptide can also be used to detect a ubiquitin conjugating enzyme polypeptide or PMI polypeptid sequence 101 AA;
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens sentrin-1 polypeptide.
sentrin-1; protection; tumour necrosis factor; tnf; apoptosis;
Fas/APO-induced; tumour cell death; induction; tumour aggressiveness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulating the production of a T-helper type 2 associated cytokine. Especially the method is useful in the inhibition of Th2 in allergy, cancer or infections, and promotion of Th2 in autoimmune disease and
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Sequence 412 F
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                                                                                                                                                                                                        New isolated sentrin
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Query Match

Local Similarity

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                         PT diagnosis of cancer and inflammation, and for promoting DNA repair
PT diagnosis of cancer and inflammation, and for promoting DNA repair
PT claim 1; Fig 1A-B; 55pp; English.

CC This represents a human SWT3-like protein (HSWTH). Host cells transformed
CC with expression vectors containing the HSWTH nucleic acid are used for
CC the recombinant production of the protein. HSWTH, expressed in cDNA
CC libraries associated with foetal development inflammation, cancer and
CC radiation damage, is used to promote DNA repair (before, during or after
CC exposure to damage from radiation or carcinogenic compounds). The
CC polypeptide can be used to treat patients with ataxia telangiectasia, or
CC related diseases, who are undergoing radiation treatment for cancers
CC associated with these diseases, or it is added to sunscreening for
CC specific binding agents (potential therapeutics). Antagonists are used to
CC treat or prevent cell proliferative diseases, especially cancer and
CC inflammation (e.g. asthma, Crohn's diseases, especially cancer and
CC inflammation (e.g. asthma, Crohn's disease, especially cancer and
CC inflammation (e.g. asthma, Crohn's disease, rhemmatoid arthritis). The
CC Exposure to acid and its fragments are used as antisense/ribozyme
CC isolating related sequences and for chromosome mapping. The antibodies
CC are used directly as therapeutic antagonists for delayors to
CC cells expressing HSWTH; as immunoassay reagents for diagnosis or
CC consitoring disease or treatment; in competitive drug screens and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human SMT3-11ke protein (HSMTH).

HSMTH; SMT3-11ke protein; recombinant; foetal development; inflammation cancer; radiation; DNA repair; carcinogenic; ataxia telangiectasia; sunscreen; therapeutic; cell proliferative disease; antagonist; asthma; crohn's disease; rheumatoid arthritis; ribozyme; chromosome mapping;
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Human secreted protein encoded by gene 47 clone
Human; secreted protein; testis; tumour; foetal
fusion protein; cancer; central nervous system;
diagnosis; neurodegenerative disease.
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Similarity 31.6%;
25; Conservative
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label= unknown
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d. No. 2.99e-02;
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brain tissue;
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New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders (Claim 1; Page 566-567; 721pp; English.

This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 47 from the human cDNA clone HOGAV75 (deposited as clone ATCC 97899 and ATCC 209045).

The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. V59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.

Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Eerner P, Ferrie AM, Fischer CL, Florence KA, Greene J, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                          Ruben SM, Shi Y, S
WPI; 98-506364/43.
N-PSDB; V59557.
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US-047618.
US-047618.
US-047633.
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US-056892.
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US-047600.
US-047601.
US-047612.
US-047613.
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JM, Hu JS,
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PT New fusion proteins resistant to proteolytic degradation -
promprising a core protein with a stabilising polypeptide comprising
promprising a core protein with a stabilising polypeptide and is the FIGA insert of the
Disclosure; Fig 3; 120pp; English.

This represents a stabilising polypeptide and is the FIGA insert of the
invention. The invention provides a method for increasing the resistance
of a core protein to proteolytic degradation that comprises linking or
comparison or into the core protein a stabilising polypeptide of
comparison or into the core protein a stabilising polypeptide of
comparison or fir and n can be anything between 1-66 x, Y and Z need not
compended to a repeat to n repeat. Alternatively a nucleic acid
compositing the stabilising polypeptide can be linked onto or inserted into
comparison are more resistant to degradation by proteases and, thus, have
compared the core protein may be an inappaB regulator protein for the
comparison of inflammatory bowel disease, or a nitroreductase protein
comparison of the core protein may be an inappaB regulator protein for the
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28-MAY-1998.
17-NOV-1997; IB1508.
25-JUN-1997; US-048945.
15-NOV-1996; US-030986.
(MASU/) MASUCCI M G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGA insert stabilising polypeptide.

Fusion protein; stabilising polypeptide; proteolytic degradation;
resistance; half-life; autoimmune disease; inflammation; nitro drug;
IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masucci MG;
WPI; 98-312463/27.
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cancer; pathological condition.
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                                     144 rgrrgrsrrgr-srrgrsrrgrsrrgrsrrgrsr 174
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                                                                                                                                                                                                 Local Similarity
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ilarity 28.6%;
Conservative
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larity 53.1%;
Conservative
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                                                                                                                                                       Score 122; DB 35; 1
Pred. No. 2.74e+00;
7; M1smatches 7;
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31-MAY-1996; U08853.
31-MAY-1995; US-455073.
(UYPE-) UNIV PENNSYLVANIA.
                                                                  TW-243453-A.
21-MAR-1995.
02-JUL-1992; 105242.
12-JUN-1992; US-899068.
(AMCY ) AMERICAN CYANAMID C
WPI; 95-214006/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 63-65; 75pp; English.

CYRI (W09429) and FXR2 (W09430) respectively show 86% and approx.

FYRI (W09429) and FXR2 (W09430) respectively show 86% and approx.

60% amino acid identity to FMR1, the protein associated with

Fragile X syndrome. They are encoded by cDNA clones (T47705-06)

obtd. from human cDNA libraries. FXR1 and FXR2 recombinant

polypeptides can be produced in transformed host cells and used

to produce FXR1- or FXR2-specific antibodies that can be utilised

in methods for screening individuals for FMR1 deficiency and

hence mental retardation caused by Fragile X syndrome.
sequences
Claim 1; Fig 2; 45pp; Chinese.
Q95540 encodes R78519, the nov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human FRX2 polypeptide.

FRX1; FRX2; FMR1; Fragile X syndrome; mental retardation; diagnosis; transgenic mouse; knockout mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09430 standard; Protein; W09430; 
20-MAY-1997 (first entry)
                                      N-PSDB; Q95540. Cardiac adenylyl cyclase and corresp.
                                                                                                                                                           Cardiac adenylyl cyclase.
Cardiac adenylyl cyclase;
                                                                                                                                                                                       R78519;
31-JAN-1996 (first entry)
                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                 R78519 standard; Protein; 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fragile X related genes FRX1 and FRX2 - used to develop for identifying individuals with mental retardation caused be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragile X syndrome
                                                                                                                                                                                                                                                                                                                                          471 rdpptrgeesrrrptggrgrgpppaprptsrynsssissvlkdpdsnpyslldtsep-ep 529
                                                                                                                                                                                                                                                                                             530 pvdsepgeppp
                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                           / Match 4.0%;
Local Similarity 32.4%;
les 23; Conservative
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                                                                                                                                                                                                                                                                     PVARLPAPAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                   673 AA;
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171
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     the novel effector
                                                                                                                                                               effector enzyme
                                                                                                                                                                                                                                                                                                                                                                          Score 113;
Pred. No. 1.
18; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                             Mismatches 26;
                                            DNA .
                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
.01e+01;
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     enzyme cardiac adenylyl
                                         having specified
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RESULT ROOM OF CO.
     PARFORMETT FOR KERRE PRESTREET FOR THE PRESTREET
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                            ULT 9
W68479 standard; 1
W68479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid mol. encoding Cardiac adenylyl cyclase type V - useful for determining and modifying cardiac function Claim 4; Page 15-27; 38pp; English.

Left ventricular tissue of canine heart was used as a source of mRNA. A cDNA library was prepd. in lambda gt10 phage. A 970 bp Aat-HincII fragment from type I adenylyl cyclase cDNA was used as probe. The clones isolated were used to obtain cDNA encoding CACV. This probe may also be used to screen a human cardiac cDNA library to obtain the cDNA encoding human CACV. CACV, its analogues and antibodies are useful in therapy or diagnostic assays, e.g. in modifying and determining cardiac function. A decrease in CACV content of the heart contributes to impaired cAMP prodn. and in heart failure. The CACV can also be used to screen for cpds. which stimulate or inhibit
                                                                                                                                                                                                                                                        08-DEC-1998 (first entry)
HIV-1 strain YBF30 rev protein.
HIV-1 strain YBF30; antibody; oligonucleotide;
infection; typing; rev.
Human immunodeficiency virus type 1.
Key
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Sequence
12-JUN-1998.
09-DEC-1996; 015087.
09-DEC-1996; FR-015087.
09-DEC-1996; FR-015087.
(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
(INRW ) INSERM INST NAT SANTE & RECH MEDICA
(INRY ) INSERM INST PASTOUR.
(INSP ) INST PASTOUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMCY ) AMERICAN CYANAMID Ishikawa Y, Konski AF; WPI; 93-068688/09.
                                                                                                                                                                     FR2756843-A1.
                                                                                                                                                                                                                                            Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q37543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1992;
29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cardiac adenylyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R32882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R32882 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 3.8%;
Similarity 50.0%;
19; Conservative
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19; Conservative
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                                                                                                                                                                                                /note=
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Pred. No. 1.77e+01;
9; Mismatches 8
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Pred. No. 1.77e+01;
9; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                               immunisation;
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Best Local S
Matches 2
                                                                                                                                                                                WO9617867-A1.
13-JUN-1996.
08-DEC-1995; U16216.
09-DEC-1994; US-353700.
(FOXC-) FOX CHASE CANCER CE
(UYTE-) UNIV TECHNOLOGIES I
RAttner JB, Yen TJ;
WPI; 96-287116/29.
N-PSDB; T34578.

NA encoding kinetochore protein for detection of malignant disease of a cell cycle, partic. for detection of malignant disease of a cell cycle. It is the product of a cDNA clone (T34578) is detected by immunofluorescence microscopy only during the G2 and M phases of a cell cycle. It is the product of a cDNA clone (T34578) isolated from a breast carcinoma cDNA library. Recombinant CENP-F can be produced by expression in prokaryotic or eukaryotic host cells. CENP-F can be used to detect autoimmune antibodies to the protein, which may provide an early diagnosis for the onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 42; 85pp; French.

Claim 9; Page 42; 85pp; French.

This sequence represents the rev protein from the non-M (major), non-O (Outlier) HIV-1 strain YBF30 (CNCM 1-1753), isolated from the Cameroon.

The HIV strain (see v60751 for complete genome), peptides, antibodies and oligonucleotides derived from it (see v60752-v60798 and w68473-w68482) are used for diagnosis of or immunisation against non-M, non-O HIV-1 infections. The oligonucleotides, peptides and antibodies can also be used for typing HIV strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 98-33b114,
N-PSDB; V60759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinetochore protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1996 (first entry)
Kinetochore protein CENP-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R99795 standard;
R99795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-M, non-O HIV-1 strain YBF30 - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEQDS-DSDSEGAAEGPAGAPRTLV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGARRARGARGRCPRARQSPARLIPDTVLVDLVSDSDEEVLEVADPVEVPVARLPAPAK 74
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98-336114/30.
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llarity 27.1%;
Conservative
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1620..17
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/note= "the C-terminal domain

form a proline-rich (10.6%)

basic (pI 10) globular domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Globular_domain
/note= "globular domain consists
repeats of 95 amino acids"
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                                                                                                                                                                                                                                                                                                                                                                                               /label= Extended_coiled_structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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Pred. No. 2.
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.70e+01;
                                                                                                                                                                                                                                                                                                                                                  domain is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                            in is predicted highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
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                                                     Recombinant CENP-F
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                     10-OCT-1996.

04-APR-1996; U04454.

03-APR-1996; US-630915.

07-APR-1995; US-417872.

(CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitomycin-C resistance; mcr locus; DNA alkylating DNA cleavage agent; drug resistance. Streptomyces lavendulae. W0509926-A. 13-ADB-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of vari
                                                                                                                                                                                                                             Mouse SH3P12 protein.

Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anticancer agents
Disclosure; Fig.2; Illpp; English.
Disclosure; Fig.2; Illpp; English.
A 3.2 kb fragment from pDHS3003 including the mcr locus of lavendulae B619 was cloned into pUC119 and sequenced. The included 3 coding sequences, mcrA, mcrB and mcrORF3. Both B are needed for high level resistance to mitomycin-C.
                                                                                                                                                       Mus musculus.
WO9631625-A1.
                                                                                                                                                                                                                                                                                                                                                                                    r 12
W05393 standard; Protein; 788
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N-PSDB; Q87790.
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                                                                                                                                                                                                          cellular signal transduction
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07-OCT-1993; US-133963.
  (UYNC-)
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nes 26; Conser
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t PR, Flickinger MC,
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Similarity 29.1%;
30; Conservative
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llarity 26.5%;
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Pred. No. 2.35e+01;
23; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 103; DB 13;
Pred. No. 4.11e+01;
21; Mismatches 48
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ance of tumour cells or as potentia
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cc identifying polypeptides containing functional domains of interest cc (especially SH3 domains). The method comprises contacting a multivalent cc recognition unit (RU) complex with a number of peptides and identifying cc polypeptides having a selective binding affinity for the RU complex. The method is finited success for identifying cc similarities. Prior methods only gave limited success for identifying cc similarities. Prior methods only gave limited success for identifying cc proteins which contain an SH3 domain due to the minimal sequence homology cc mamong known SH3 proteins. It has been found that small peptide RUs in cc mmpared to monomer RUs. Multivalent RU complexes are particularly suited to screening for polypeptides containing functional domain cc compared to monomer RUs. Multivalent RU complexes are particularly suited to screening for polypeptides containing functional domains that are cf unctional domain. The new method enables proteins having a common cc function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal custoff their specificities (e.g. pharmacological activities) can be assessed compand that the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying polypeptide(s) having specific functional domain (esg SH3 domain) - comprises detecting selective binding to recognition unit, regardless of sequence homology claim 54; F1g 43; 174pp; English.

W05386-W05403 represent novel human and mouse Src-homology region domain containing proteins that can be used in the method of the invention. SH3 domain containing proteins that can be used in the invention is for structural elements of cells. The method of the invention is for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T39793
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Length 788;
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Query Match 3.6%; Best Local Similarity 22.3%; Matches 39; Conservative 232 262 176 203 121 143 splsvprsksemnyiegekvvkrsatl-plpars-sslkssperndwepldkkvd QSPALQSTDDEVVLVEGP-VLPQSSRLFTLKIRCRADLVRLPVRMS-EPLQNVVD VQSSLNLIPDNSSLLK-LCP-SEPEDEADLTNSGSSPSEDD-ALPS-GSPWR-KKLRKKC 175 vnptivllqhnreqqkrlsslsdpaserrageqdpvptpaeltspgraserrakdasrrv 202 EKEEKKMEEFPDQDIS-PLPQPSSRNKSR-KHT-EALQKL-REVNKRLQDLRSCLSPKQH vrsaqdlsdvstdevgiplrn-terskdwyktmfkqihklnrdddsdvhsprysfsddtk 261 Score 102; DB 25; Pred. No. 4.71e+01; 46; Mismatches 76: 76; Indels 14; 314 Gaps 231 14;

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New DNA encoding infectious rubella virus - esp. non-pathogenic mutant virus for use in vaccines having reduced side effects Disclosure; Columns 17-28; 27pp; English.

Non-pathogenic mutants of the DNA corresponding to this sequence are useful in vaccines (which may include epitopes from other viruses). The mutant vaccines are less likely to cause foetal infections, autoimmune disease or neurological symptoms, so can be administered safely to older or pregnant women. The mutant sequence is
                                                                                                                        Dominguez G, Frey TK, WPI; 95-283097/37. N-PSDB; 097686.
                                                                                                                                                                                                                                                                                                                                               R79048
R79048;
                                                                                                                                                                     28-JUN-1991; 722334.
28-JUN-1991; US-722334.
19-JUL-1993; US-093453.
19-JUL-1993; US-093453.
                                                                                                                                                                                                                                                                  pregnancy; foet
Rubella virus.
                                                                                                                                                                                                                                                                                  Infectious rubella virus N-terminal transcript.
Rubella; vaccine; mutant; epitope; virus; autoimmune disease; pregnancy; foetal infection; vector; plasmid.
                                                                                                                                                                                                                                                     US5439814-A.
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                                                                                                                                                                                                                                                                                                                  This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain Bg8090. Comparison of the N-terminal and central regions (M14533-57 and W14562-91) of PspA polypeptides from different commococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as of this media, menigitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine Sequence 213 AA;
                                                                                                                                                                                                                                                                       Query Match
Best Local
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16-SEP-1995; U14819.
15-SEP-1995; US-529055.
(UABR-) UAB RES FOUND.
Briles DE, Brooks-Walte.
W18664; standard; Protein; 386 AA.
W18664;
24-JUL-1997 (first entry)
24-JUL-1997 (first entry)
Fragmented human NF-H gene +1 frameshift mutant product.
Frameshift mutation product; GAGA motif; somatic mutation; diagno:
detection; antibody; probe; cancer; neoplasia; neurodegenerative;
parkinson's; Alzheimer's disease; Pick's; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae PspA central region. PspA; pneumococcal surface protein; vaccine; meningitis; bacteraemia; pneumonia. Streptococcus pneumoniae strain Bg8090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Briles DE, Brooks-Walter A, McDaniel LS, Swiatlo E, Tar WPI; 97-202002/18.
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W14567 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preferably present in a vector, especially allows replication of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae surface protein PspC and truncated PspA used in vaccines for protecting animals against S pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9709994-A1.
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Pred. No. 4.71e+01;
17; Mismatches 48
                                                                                                                                                                                                                                                   Score
Pred.
12; M
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                                                                                                                                                                                                                                                                     99; DB 24;
No. 7.12e+01
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                                                                                                                                                                                                                                                                                    Length 213;
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                                           diagnosis
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PLR-GRGPRSRGGRGARRARGARGRCPRA

31

Search completed: Fri

18

time :

94

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pridiseases, e.g. cancer or neuroidegenerative disease

Sclaim 22; Fig 9; 132pp; English.

CC W18663 and W18664 are +2 and +1 frameshift mutations, respectively,

CC of a sequence comprising fragments of the coding sequence of the

Numan neurofilament subunit NF-H gene corresponding to nucleotides

CC inla2 of the wild-type NF-H gene. This region contains GAGAG motifs.

CC Frameshift mutants of the tau, ubiquitin, apolipoprotein E,

CC microtubule-associated protein 2 (MAP-2), neurofilament subunit L, M

CC and H and amyloid A4 genes are claimed. All these genes share a common

CC dinucleotide deletion(s) that cause neurodegenerative disorders.

CC dinucleotide deletion(s) that cause neurodegenerative disorders.

CC dispins prevention and treatment of cancer and neurodegenerative

CC diseases, e.g. Parkinson's disease, Alzheimer's disease, Down's

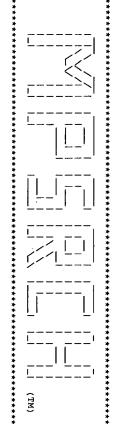
CC supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's

CC disease, multiple sclerosis, and other degenerative diseases such as

CC cardiovascular disease and rheumatoid arthritis.
                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI. (UYRO-) UNIV ROTTERDAM ERASMUS. (UYUT-) UNIV STATE UTRECHT. BURDACH JPH. GROSVELD FG, Van Leeuwen FW WPI: 97-226235/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Down's syndrome; frontal lobe dementia; progressive supranuclear palsy; PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS; cardiovascular; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of mutant genes having frame:shift mutation(s) - for develop prods. for the diagnosis, prevention and treatment of associated diseases, e.g. cancer or neuro:degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
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02-OCT-1995; GB-020080.
11-JAN-1996; US-009832.
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231 plrygravrargprdarrg-aapgrgars
                                                                                                       Local
                                                                                                         Similarity
                                                                               16;
                                                                         3.5%;
larity 55.2%;
Conservative
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production"
                                                                                                       Score 100; DB 22; Pred. No. 6.21e+01;
                                                                               6;
                                                                               Mismatches
                    258
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. Fri Feb 18 12:02:02 2000; MasPar time 7.55 Seconds 706.764 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-08-755-584-2 (1-412) from 5858711.pep 2858 1 MAEPLRGRGPRSRGGRGARR.....GKELPADLGLESGDLIEVWG 412

Scoring table: РАМ 150 Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Mean 32.940; Variance 177.353; scale 0.186

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		,						
No.	Score	Query Match	Query Match Length	DB	ID	Description		Pred. No.
1	2858	100.0	412	N		Sequence 2,	Applicatio	
2	160	5.6	104	N	6	Sequence 3,	Applicatio	e-0
ω	152	5.3	126	N	-80-	Sequence 1,	ը	Մ
4	113		673	N			Б	5.18e+00
σı	106	٠	265	N	-80-	Sequence 1,	ř	•
on	107	3.7	3248	ω	PCT-US95-1	Sequence 1,	բ	:،
7	107	٠	3248	Н	US-08-353-	Sequence 1,	բ	.21e+0
æ	102	•	2205	ш	- 1	æ	Applicatio	. 44
9	100		181	N	us-08-726-	W	, Applicati	.21e+0
10	99		397	ω	PCT-US96-1	10	Applicatio	.69e+0
11	99	•	568	ω	PCT-US94-0	Sequence 30	, Applicati	.69e+0
12	99	٠	568	ш	US-08-320-	10	, Applicati	3.6
13	98		30	Ļ	US-08-218-		잂	4
14	97	3.4	123	N	US-08-306-	Sequence 5,	Applicatio	4
15	97	3.4	123	N	US-08-240-	Sequence 1,	Applicatio	
16	. 97	3.4	166	ب	7	,,,	\vdash	
17	97	3.4	166	ω	PCT-US93-0		\vdash	
18	97	3.4	166	ᆫ	US-08-368-	Sequence 2,	Applicatio	4.85e+01
19	98	3.4	237	N	US-08-970-	Sequence 5,	\vdash	22
20	97	3.4	359	N	US-09-092-		Applicatio	
21	96	3.4	359	N			\vdash	i.n
22	96	3.4	389	N	US-08-802-	Sequence 14	, Applicati	.55e
23	97	3.4	404	N		Sequence 3,	Applicatio	'n

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
92	92	92	92	94	94	94	94	94	93	93	93	94	94	94	95	95	95	96	96	96	96
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ALIGNMENTS

888888888888888888888888888888888888888	*##	RESULT ID U XX AC x XX DT
ZIP: 02109-1875 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/755,584 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: J1.53 PRIOR APPLICATION NUMBER: #ITORNEY/AGENT INFORMATION: REGISTRATION NUMBER: #11.026 TELECOMMUNICATION NUMBER: HUI-026 TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400 INFORMATION OF SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 412 amino acids TYPE: amino acid	Sequence 2, Application US/08755584 Sequence 2, Application US/08755584 Patent No. 5858711 GENERAL INFORMATION: APPLICANY: Glimcher, Laurie H. APPLICANY: Glimcher, Laurie H. APPLICANY: Hodge, Martin R. TITLE OF INVENTION: NF-AT-INTERACTING PROTEIN NIP45 AND METHODS TITLE OF INVENTION: OF USE THEREFOR NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIYE & COCKFIELD STREET: 60 State Street, suite 510 CITY: Boston STATE: Massachusetts COUNTRY: USA	LT 1 US-08-755-584-2 STANDARD; PRT; 412 AA. XXXXXX

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Best Local :
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SEQUENCE 412 AA;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08853974
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-853-974-3
                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08853974
Patent No. 5840534
GENERAL INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
FITING PATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                     APPLICATION NUMBER: US/08/8 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN SMT3-LIKE PROTEIN NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                              APPLICANT: Hillman, Jennifer L. APPLICANT: Shah, Purvi
                                                                                                                                                                                                   STREET: 31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMEEFPDQDISPLPQPSSRNKSRKHTEALQKLREVNKRLQDLRSCLSPKQHQSPALQSTD 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGESELSPTATPSTLKLGVADIIDCVVLASSSEATETSQELRLRVQGKEKHQMLEISLSP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVVLVEGPVLPQSSRLFTLKIRCRADLVRLPVRMSEPLQNVVDHMANHLGVSPNRILLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVEVPVARLPARPEQDSDSDSEGAAEGPAGAPRTLVRRRRRRLLDPGEAPVVPVYSGK 120
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                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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3174 Porter Drive
                                                                                                                                                                                        USA
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                                                                               US/08/853,974
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Pred. No. 2.34e-214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08853974
                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 ETSQELRLRVQGKEKHQMLEISLSPDSPLKVLMSHYEEAMGLSGHKLSFFFDGTKLSGKE 395
                                                                                                                                                                                                                                                                                                                                                              Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 LPADLGLESGDLIE 409
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Sheh, Purvi
TITLE OF INVENTION: HUMAN SMT3-
      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 DGGAHINLKYKGQDGNEYF-FRIKRSTQLKKLMNAYCDRQSVDMNSIAFLFDGRRLRAEQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 TPDELDMEDGDEID 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                       APPLICATION NUMBER: US/08/8: FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1707372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
                                               REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                            STREET: 3174 Po:
CITY: Palo Alto
STATE: CA
                                      TELEPHONE:
                                                                                                       FILING DATE:
                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6%;
Similarity 25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 AA; 11654 MW; 46917 CN;
                                                                                                                                                                                                                                                                                                                                                     , Application US/08853974 5840534
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126 amino acids
                                                                                                                                                                                                                                                                   3174 Porter Drive
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                             415-845-4166
                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                        415-855-0555
                                                                                                                                                                                                                                                                            Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                             HUMAN SMT3-LIKE PROTEIN
                                                                                                                                                US/08/853,974
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Pred. No. 4.58e-03;
26; Mismatches 28
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 Query Match 4.0%;
Best Local Similarity 32.4%;
Matches 23; Conservative
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Best Local
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STRANDEDNESS: Single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGFET03
CLONE: 2361410
SEQUENCE 126 AA; 13961 MW; 87522 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
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                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5876949
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                  TELEFAX: (215) 568-34 INFORMATION FOR SEQ ID NO:
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                              TYPE: ama...
STRANDEDNESS:
TOPOLOGY: linear
TOPOLOGY: 74079
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      REFERENCE/DOCKET NUMBER: UP TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 31-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gideon Dre
APPLICANT: Mikiko C.
APPLICANT: Yan Zhang
                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods TITLE OF INVENTION: Of Making And Using The Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGKELPADLGLESGDLIEV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NETDTPAQLEMEDEDTIDV 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGVKTENDHINLKVAGQDGS-VVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPI 66
                                                                                                                                                                          NAME: DeLuca, Mark REGISTRATION NUMBER:
                                                                                           LENGTH: 673 amino acid residues
                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 5.3%;
Similarity 31.6%;
25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                One Liberty Place,
                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gideon Dreyfuss
Mikiko C. Siomi
                                              74079
                                                                                                                                                                                                                   31-MAY-1995
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                                                                                                                             568-3439
                                              WW;
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                                                                                                                                                                       33,229
Score 113; DB 2; L6
Pred. No. 5.18e+00;
18; Mismatches 26;
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Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 152; DB 2;
Pred. No. 1.57e-02;
19; Mismatches 33
                                              2221704 CN
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                       Length 673;
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                                                                          Query Match 3.7%;
Best Local Similarity 28.6%;
Matches 22; Conservative
                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXX
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            97
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 PVARLPAPAKP 75
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/9: FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                    IMMEDIATE SOURCE:
SLDHKLAEVSQNIEKLR 113
                                              NKGATPEDFSNLPPE-QRRKKLQQKVDELNKEIQKEMDQRDAITKMKDVYLKNPQMGDPA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                        LIBRARY: bit...

CONF. 865744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDPPTRGEESRRRPTGGRGRPPPAPRPTSRYNSSSISSVLKDPDSNPYSLLDTSEP-EP 529
                                NSGSSPSEDDALPSGSPWRKKLRKKCEKEEKKME-EFPDQD-ISPLPQPSSRNKSRKHTE 207
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                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                      NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                             LENGTH:
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                                                                                                                   265 AA; 30106 MW; 347009 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palo Alto
                                                                                                                                                                                   amino acid
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                                                                                                                                                                                             265 amino acids
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Guegler, Karl J.
Lal, Preeti
Lal, Preeti
VENTION: SH3-CONTAINING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                              linear
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                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                    36,749
                                                                         Score 106; DB 2;
Pred. No. 1.39e+01
21; Mismatches 3
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                                                 RESULT
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Best Local :
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             XXXXXX
                                    US-08-353-700-1
                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                  177 KEEKKMEETPDQDISPLPQPSSRNKSRKHTEALQKLREVNKRLQDLRSCLS-PKQHQSPA 235
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                                                                                    236 LQSTDDEVVLVEGPVLPQSSRLFTL-K-I-RCRADLVR 270
                                                                                                          90 LOVKESOVNFOEGOLNSGKKOIEKLEOELKRCKSELER 127
                                                                                                                                                          31 KKEKQQRQFQLDSLEAAPQKQTQKVENEKTEG-TNLKRENQRLMEICESLEKTKQKISHE 89
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                  3.7%;
Local Similarity 26.5%;
cos 26; Conservative
                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
JENCE 3248 AA; 372207 MW; 51689535 CN;
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/3
FILING DATE: 09-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yen, Timothy J.

APPLICANT: Rattner, Jerome B.

TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1601 Market
CITY: Philadelphia
                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: no
TOPOLOGY: not re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                   3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                not relevant
                                    STANDARD;
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                                                                                                                                                                                Score 107; DB 3;
Pred. No. 1.21e+01;
23; Mismatches 44
                                    PRT;
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                                    3248
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                                                                                                                                                                                                        Length 3248;
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Best Local S
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                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                              Sequence 2, Application US/08093453B
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          Sequence 2, Application US/08093453B Patent No. 5439814
                                                                                                                                                                                                                     177 KEEKKMEEFPDQDISPLPQPSSRNKSRKHTEALQKLREVNKRLQDLRSCLS-PKQHQSPA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1,
                                                                                                                                                                     236 LQSTDDEVVLVEGPVLPQSSRLFTL-K-I-RCRADLVR 270
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GENERAL INFORMATION:
                                                                                                                                                                                             90 LQVKESQVNFQEGQLNSGKKQIEKLEQELKRCKSELER 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                           31 KKEKQQRQFQLDSLEAAPQKQTQKVENEKTEG-TNLKRENQRLMEICESLEKTKQKISHE 89
                                                                                                                                                                                                                                                                              Match 3.7%;
Local Similarity 26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (215) 563-40.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RATTNER, J
TITLE OF INVENTION: N
TITLE OF INVENTION: T
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOSIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELECHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFMAN, HERRELL AND STREET: 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                   ORGANISM: HUI
ICE 3248 AA;
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1601 MARKET
CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                    26;
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              3248 amino acids
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                                                                                                                                                                                                                                                                                                                                HUMAN
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                                                                                                                                                                                                                                                                                                                   372207 MW; 51689535 CN;
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563-4044
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                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                 Score 107; DB 1;
Pred. No. 1.21e+01;
23; Mismatches 44
                                                                                                                      PRT;
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                                                                                                                      2205 AA
                                                                                                                                                                                                                                                                    44; Indels
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KINETOCHORE PROTEIN,
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REFERENCE/DOCKET NUMBER: 0736:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404_818-3709
TELEPAX: 404_818-3799
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2255 amino acids
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                            US-08-726-306A-56
                                                                                                                                                                                                               2145 LLPFGRAPGCPNGFYYPHHHG-GPPEGPRGTIPRPARGTRRRRLABAPAAA 2194
                                                                                                                                                                                                                                                              2086 GARPRPPGHHRRARGDSDP-LRARQSPRRRLTPLYVGPLILPTLTRSSPTVVSPHLVGTQ 2144
                                                                      Sequence 56, Application US/08726306A
                                                                                                                    XXXXXX
                       Sequence 56, Application Patent No. 5958684 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                           63 EVPVARLPAPAKPEQDSDSDSEGAAEGPAGA-PRTLVRRRRRLLDPGEAP
                                                                                                                                                                                                                                        9 GPRSRGGRGARRARGARGRCPRARQSPAR-LIP---DT-VLVDLVSDSDEEV-LEVADPV 62
                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N_terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/722,334
FILLING DATE: 28 JUN 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Frey, Teryl K.
APPLICANT: Dominguez, Geraldina
APPLICANT: Wang, Chin_Yen
TITLE OF INVENTION: Modified Infectious Rubella Virus
NUMBER OF SEQUENCES: 13
                                                                                                                                                          ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Kubu
ORGANISM: Therien
240
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/093,453B FILING DATE: 19 JUL 1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: MacIntosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                        h 3.6%;
Similarity 33.3%;
37; Conservative
                                                                                                                                                                                                                                                                                                                                       2205 AA; 240235 MW; 22500019 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greene, Jamie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Jamie L. Greene, Jones & Askew 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States
van Leeuwen, Frederik Willem
Burbach, Johannes Peter Henr:
                                                                                                                                                                                                                                                                                                                                                              Rubella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
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                                                                                                                                            STANDARD;
                                               US/08726306A
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                                                                                                                                           PRT;
                                                                                                                                           181 AA
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                                                                                                                                                                                                                                                                                                               Length 2205;
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                Sequence 6, Applications GENERAL INFORMATION:
APPLICANT: The Ge
STATE: MA
COUNTRY: USA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                              42 PLRYGRAVRARGPRDARRG-AAPGRGARS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 345-9111 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         4 PLR-GRGPRSRGGRGARRARGARGRCPRA
                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Alchardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
JENCE 181 AA; 17613 MW; 98529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,380
REFERENCE/DOKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/009,832
FILING DATE: 01-Jan-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
                                                                                                                    APPLICANT: The General Hospital Corporation TITLE OF INVENTION: INHIBITION OF HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grosveld TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                       STREET: STREET: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                    h 3.5%;
Similarity 55.2%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boston
                                                                                                                                                      Application PC/TUS9610602
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                                                                                                                                                                                                                                                                                                                                                                                                                                     181 amino acids
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1 Financial Center
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                                                                                                                                                                                                                                             STANDARD;
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                                                                                     Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/726,306A
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Pred. No. 3.21e+01;
...amatches 5;
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                                                                                                                                                                                                                                             PRT;
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Best Local
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 397 amino acids
                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application PC/TUS9404496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US94-04496-30
                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application PC/TUS9404496 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 RGRSPRRT-PSPRR-R--RSQSPRRRRSQSRLGPLLVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0076
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Φ
                                                                                                                                                                                                                                           APPLICANT: Croce, Carlo
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
         ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein 946620 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGRGPRSRGGRGARRARGARGRCPRARQSPARLIPDTVL 44
                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                STREET: One Liberty Place, CITY: Philadelphia
                                                                                                                                                                                                                         ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/0 FILING DATE: 20-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
REFERENCE/DOCKET NUMBER:
                                                CLASSIFICATION:
                                                              FILING DATE
                                                                        APPLICATION NUMBER:
                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                              19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                    Pennsylvania
                                                                                                                                                                          USA
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PatentIn Release #1.0, Version #1.30
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Pred. No. 3.69e+01;
7; Mismatches 9
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 TJU-1242
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   FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
                                              FILING DATE: 30-OCT->-
FILING DATE: 30-OCT->-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
APPLICATION NUMBER: 27-MAX-92
                                                                                                                                                                                                                                                                                                 STATE: I
                                                                                                                                                                                                                                                                                        ZIP: 19103
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DeLuca,
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FILING DATE:
FILING DATE:
CLASSIFICATION: 435
CRASSIFICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
TITING DATE: 30-OCT-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30, Application US/08320559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 SFSKP-HK-LMKE-HKE-KPSKDSREHK-SAFKEPS-RDHNKSSKESSKKPKE-NKPLKE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 RRRLLDPGEAPVVPVYSGKVQSSLNLIPDNSSLLKLCPSEPEDEADLTNSGSSPSEDDAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 Match 3.5%;
Local Similarity 26.7%;
les 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                          SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein JENCE 568 AA; 63367 MW; 1762870 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                              COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Application US/08320559
5633135
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                                                                                                                                                                                                                                                                                           IBM PS/2
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                                                                                                                                                                                                                                                                      PC-DOS
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Pred. No. 3.69e+01
32; Mismatches 4
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                                                                                                                                                                                                                                                                                                               3.5 INCH, 1.44 Mb STORAGE
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                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08218608
                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 PSGSPWRKKLRKKCEKEEKKMEEFPDQDISPLPQPSSRNKSRKHTEALQKLREVNKRLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 SFSKP-HK-LMKE-HKE-KPSKDSREHK-SAFKEPS-RDHNKSSKESSKKPKE-NKPLKE 244
                                                                                                                                                                                                                                                                                                                         Patent No. 5607859
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 RRRLLDPGEAPVVPVYSGKVQSSLNLIPDNSSLLKLCPSEPEDEADLTNSGSSPSEDDAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%;
Local Similarity 26.7%;
les 32; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215) 568-343
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acid
                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
                                                                               ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: M00
                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                               APPLICANT: BIEMANN, KLAUS APPLICANT: JUHASZ, PETER TITLE OF INVENTION: METHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                    TELECOMMUNICATION INFORMATION:
                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                    STREET: 600
CITY: BOSTO
STATE: MA
COUNTRY: US
ZIP: 02210
                                                                                                             TILING DATE: 28-MAR-1994
CLASSIFICATION: 436
FTORMEY ASSETS
                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
       STRANDEDNESS:
                                                              TELEPHONE:
                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LE TYPE: protein
568 AA; 63367 MW; 1762870 CN;
                                                                                                                                                                                                                                                                                                                                    0, Application US/08218608 5607859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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             : 30 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 amino acids
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                                                   617-720-3500
617-720-2441
                                                                                                                                                                                                              USA
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     single
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                  GREENFIELD & SACKS, P.C
                                                                                                                                                                                                                                                                     METHODS AND PRODUCTS FOR MASS
SPECTROMETRIC MOLECULAR WEIGHT DETERMINATION OF POLYIONIC ANALYTES EMPLOYING POLYIONIC REAGENTS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33,229
ER: TJU-0855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.69e+ 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99; DB 1;
Pred. No. 3.69e+01
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                                                                                 M0656/7013
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                                                                                                                                                         Version #1
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Matches 2
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Best Local S
Matches 1
                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08306078
                                                                                                                                                                                                            APPLICATE: 14-SEF TILING DATE: 14-SEF TONEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Blackstone, William B.
NAME: 29,772
TOTATSTRATION NUMBER: 29,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5827646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 3.4%;
Local Similarity 62.1%;
hes 18; Conservative
                                               Local Similarity
les 28; Conse
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             21
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HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                         TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Middeldorp, Jaap Michiel JM
APPLICANT: van Grunsven, Wouterus Marinus Johannes WMJ
TITLE OF INVENTION: Diagnostic reagents for the
TITLE OF INVENTION: detection of antibodies to EBV.
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
RARG-RGRG-RGEKRPRSPSSQSSSSGSPPRRPPPGRRPFFHPVGEADYFEYHQEGGPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGRGPRSRG-GRGARRARG-ARGRCPRAR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1330 Pic
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NISM: NONE (SYNTHETIC PEPTIDE)
30 AA; 3217 MW; 2370 CN;
                                                                                                          LE TYPE: peptide
123 AA; 12990 MW; 70971 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20850-4377
                                            3.4%;
llarity 28.3%;
Conservative
                                                                                                                                                                     amino acid
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                                                                                                                                                                                     123 amino acids
                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                               EP 93202659.4
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                                                                                                                                                                                                                                                                                                                                                              US/08/306,078
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Pred. No. 4.23e+01;
4; Mismatches 3
                                            Score 97; DB 2; L
Pred. No. 4.85e+01;
26; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                               Indels
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EP-D; VPPGAIEQGPADDPGEGPSTGPRGQGDG-GRRKK

RGRGPRSRGGRGARRARGARGRCPRARQSPARLIPDT-VLVDLVSDSDE-EVLEVADPVE 63

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Search completed: Fri Feb 18 12:02:29 2000 Job time: 27 secs.
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                                                                                                                                                                          Query Match
Best Local Similarity 28.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 123 AA; 12990 MW; 70971 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08240717A
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                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/240,717A
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92.202797.4
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: GOTMLBY, MATY E.
REGISTRATION NUMBER: 34,409
TELEPHONE: (301) 258-5200
TELEPHONE: (301) 258-5200
TELEPHONE: (301) 27-0847
                                                                                      79 EP-D-VPPGAIEQGPADDPGEGPSTGPRGQGDG-GRRKK 114
                                                                                                                                  21 RARG-RGRG-RGEKRPRSPSSQSSSSGSPPRRPPPPGRRPPFFHPVGEADYFEYHQEGGPDG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Middel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 VPVARLPAPAKPEQDSDSDSEGAAEGPAGAPRTLVRRRR 102
                                                          64 VPVARLPAPAKPEQDSDSDSEGAAEGPAGAPRTLVRRRR 102
                                                                                                                 6 RGRGPRSRGGRGARRARGARGRCPRARQSPARLIPDT-VLVDLVSDSDE-EVLEVADPVE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Middeldorp, Jaap M.
TITLE OF INVENTION: Epstein Barr Virus Peptides and
TITLE OF INVENTION: Antibodies Against These Peptides
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Marviana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Pred. No. 4.85e+01;
26; Mismatches 38
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: bular output not generated. Fri Feb 18 11:57:35 2000; MasPar time 18.85 Seconds 875.682 Million cell updates/sec

Title: Description: Perfect Score: Sequence:

>US-08-755-584-2
(1-41) from 5858711.pep
2858
1 MAEPLEGEGFRSEGGEGARR.....GKELPADLGLESGDLIEVWG 412

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 49.563; Variance 122.566; scale 0.404

SUMMARIES

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109	110	109	110	109	109	110	109	109	108	111	111	113	115	115	114	113	117	125	129	152	161	Score
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1184	657	596	476	431	410	385	380	340	229	1030	359	.2142	1872	1870	932	673	771	101	1402	91	95	Length
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A42904	S05517	A45195	S36513	S09824	E70579	I39498	T00792	B55973	WMAD51	S11034	I51734	B35098	S36152	S37671	A42632	S60173	B70564	S63999	146707	JC5582	JC4760	ID
adenylylcyclase type		clase typ	L2 protein - human pa	hypothetical protein	probable murG protein	н	hypothetical protein	transcription factor	late 33K protein - hu	۳	transcription factor	MHC class III histoco	bat2 protein - human	bat2 protein - human	cell adhesion molecul	fragile X mental reta	ď	SMT3 protein - yeast	initiation factor 4-g	SMT3 protein - Caenor	SMT3 protein - human	Description
2.24e+00	1.77e+00	2.24e+00	1.77e+00	2.24e+00	2.24e+00	1.77e+00	2.24e+00	2.24e+00	2.84e+00	1.40e+00	1.40e+00	8.63e-01	5.31e-01	5.31e-01	6.77e-01	8.63e-01	3.25e-01	4.34e-02	1.54e-02	2.96e-05	2.27e-06	Pred. No.

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24
104	106	105	105	106	105	107	105	107	106	107	107	105	106	106	106	106	105	110	110	108	110
3.6	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	ა	ა	3.8 8	ა
265	3414	1893	1822	1703	1234	1107	1051	913	676	676	525	358	349	349	349	349	338	2424	2424	2284	1302
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LPRB1B	GNWVNE	A56158	S33441	S15047	I38994	E65226	S27002	S20590	EDBE23	EDBE22	S36405	A55973	I50369	167417	I53277	I67418	I38587	I46479	I46480	GNVVGV	A41249
apolipoprotein A-I pr	genome polyprotein -	eye development prote		SNF2 protein - yeast	phospholipase C-beta-	hypothetical 123.8 kD	phospholipase C (EC 3	exo-alpha-sialidase (immediate-early prote	immediate-early prote	nucleocapsid protein	_	transcription factor	transcription factor	transcription factor	transcription factor	retrovirus-related le	calcium channel BI-2	calcium channel BI-2	genome polyprotein -	multidrug resistance
7.16e+00	4.52e+00	5.69e+00	5.69e+00	4.52e+00	5.69e+00	3.58e+00		3.58e+00	4.52e+00	3.58e+00	3.58e+00	5.69e+00	4.52e+00	4.52e+00	4.52e+00	4.52e+00	5.69e+00	1.77e+00	1.77e+00	2.84e+00	1.77e+00

ALIGNMENTS

ACCESSIONS REFERENCE #authors #journal	RESULT 2 ENTRY TITLE ORGANISM DATE	Db 71 DTPAQLE : : Qy 395 ELPADLC	12	Query Match 5.6%; Best Local Similarity 32.9%; Matches 25; Conservative	#map_position CLASSIFICATION SUMMARY	GENETICS #gene ##cross-ref	##molecule_type mRNA ##residues 1-95 ##cross-references G	#Cross-referen	#authors #journal #title	ACCESSIONS REFERENCE	RESULT 1 ENTRY TITLE ORGANISM DATE
JC5582 JC5582 Choudhury, B.K.; Li, S.S.L. Biochem. Biophys. Res. Commun. (1997) 234:788-79;	<pre>JC5582 #type complete SMT3 protein - Caenorhabditis elegans #formal_name Caenorhabditis elegans 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999</pre>	DIPAQLEMEDEDIDY 86 : : : : ELPADIGLESGDLIEV 410	TENNDHINLKVAGQDGS-VVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFREDGQPINET 70	5.6%; Score 161; DB 2; Length 95; Similarity 32.9%; Pred. No. 2.27e-06; 25; Conservative 19; Mismatches 31; Indels 1; Gaps 1;	4 #superfamily yeast SMT3 protein #length 95 #molecular-weight 10871 #checksum 3774	CS ##cross-references GDB:5752862	##molecule_type mRNA ##residues 1-95 ##label MAN ##cross-references GB:L76416	suppressor of MIF2 mutations in a centromere protein gene. ccross-references MUID:96212932	199 hom	JC4760 JC4760	<pre>JC4760 #type complete \$MT3 protein - human #formal_name Homo sapiens #common_name man 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Mar-1999</pre>

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Best Local Similarity 22.5%;
Matches 18; Conservative
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Best Local Similarity 20.8%;
Matches 46; Conservative
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#accession JC5582
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##cross-references GB:U94830; NID:g2341094; PID:g2341095
This protein is asuppressor of MIF2 mutation in a centromere
                                                                                                                                                                                                                                                                                                                                                                                                                       482 ALSSRGP-PRGGPGGELPRGAAGLGPRRSLQPRPPRGARKLIASVIMTEDIKLNKAEKAW 540
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                                                                                            180 K-KME-EFPDQDISPLPQPSSRNKSRKHTEALQKLREVNKR 218
                                                                                                                                                                                        122 QSSLNLIPDNSSLLKLCPSE-PEDEADLTNSGSSPSEDDALPSGSPWRKKLRKKCEKE-E 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GB:L22090; NID:g404774; PID:g404775
# length 1402 #molecular-weight 154049 #checksum
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                                                                                                                                                                                                                                                                                  64 VPVARLPAPAKPEQDSDSDSEGA-AEGPAGAPRTLVRRRRRLLDPGEAPVVPV-YSGKV 121
                                                                                                                                                                                                                                                                                                                                                                            4 PLRGRGPRSRGGRGARRARGARGRCPRARQSPARLIPDTVLVDLVSDSDEEVLEVADPVE 63
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                                                                                                                                          KDKDDDEVFEKKQKEMDEAATAEERERLKEELEEARDIARR 698
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J. Biol. Chem. (1993) 268:19200-19203

Mapping the cleavage site in protein synthesis initiation factor eIF-4 gamma of the 2A proteases from human coxsackievirus and rhinovirus.
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initiation factor 4-gamma - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
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#superfamily yeast SMT3 protein
#length 91 #molecular-weight 10222 #checksum
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#type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129; DB 2; Length 1402; Pred. No. 1.54e-02; 62; Mismatches 103; Indels 10;
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Pred. No. 2.96e-05;
31; Mismatches 30;
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TITLE
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#map_position 4R
CLASSIFICATION #superfamily yeast SMT3 protein
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Best Local Similarity 33.3%;
                                                                                                                                                                                                                                  #authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Murphy, L.; Oliver, S.; Squeres, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

# Hornsby Taylor, K.; Whitehead, S.; Barrell, B.G.

# Localphering the biology of Mycobacterium tuberculosis from the complete genome sequence.

# Cross-references MUID: 98295987
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                                                             ##molecule_type DNA
#*residues 1-771 ##label COL
##cross-references GB:205436; GB:AL123456;
#PID:g2105045
PID:g2105045
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**experimental_source strain YPH1/YNN214
NCE 569553
thore -:
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submitted to the EMBL Data Library, August 1995
The sequence of S. cerevisiae cosmids 8166, 9787,
lambda 3073.
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563999; S69567
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hypothetical protein Rv3649 - Mycobacterium tuberculosis
__(strain H37RV)
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17-Jul-1998
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                                                                                                                                                                              preliminary; nucleic acid sequence not shown; translation not shown
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  *molecular-weight 81409
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the EMBL Data Library, May 1995
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Pred. No. 4.34e-02;
11; Mismatches 21
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Best Local
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Dutra, A.; Nussbaum, R.L.; Dreyfuss, G.
#journal EMBO J. (1995) 14:5358-5366
#title The fragile X mental retardation syndrome
with novel homologs FXR1 and FXR2.
#cross-references_MUID:96080171
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##cross-references EMBL:(J1501; NID:g1098636; PID:g1098637
##note the authors translated the codon CTA for residue 59 as #note Thr, CTG for residue 91 as Thr, CTG for residue 164
Thr, and CTC for residue 171 as Thr
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Local Similarity 32.4%;
hes 23; Conservative
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Local Similarity 24.68;
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                                                                                                                                                                                                                   PVARLPAPAKP 75
                                                                                                                                                                                                                                                                                       RGPRSRGGRGARRARGARGR-CPRARQSPARLIPDTVLVDLV-SDSDE-EVLEVADPVEV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVVLASSSEATETSQELRLRVQGKEKHQMLEISLSPDSPLKVLMSHYEEAM
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28-Apr-1995
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fragile X mental
                                                  04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                    #formal_name Aplysia californica #common_name California
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adhesion molecule apCAM (clone
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th 673 #molecular-weight 74128 #checksum 2966
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Pred. No. 3.25e-01;
47; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                             Score 113; DB 2; L
Pred. No. 8.63e-01;
18; Mismatches 26;
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Best Local S
Matches 2
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Best Local Similarity 29.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-932 ##label MAY
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Similarity 29.5%;
28; Conservative
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#type ---.
bat2 protein - human

#formal_name Homo sapiens #common_name man
20-Feb-1995 #sequence_revision 20-Feb-1995

10-Sep-1997
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38/2; 97/2; 129/3; 154/1; 202/1; 252/3; 279/2; 327/1; 357/2; 429/3; 588/1; 651/1; 751/1; 821/2; 1436/2; 1525/1; 1568/3; 1612/1; 1640/3; 1715/3; 1762/3; 1786/3; 1842/3
#length 1870 #molecular-weight 199223 #checksum 7735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bougueleret, submitted to $37671
                                                                                 $36152 #type complete
bat2 protein - human
#formal_name Homo sapiens #common_name man
06-Jun-1995 #sequence_revision 17-Nov-1995
17-Nov-1995
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#length 932 #molecular-weight 101521 #checksum 807
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Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina,
Primas, G.; Perrot, V.; Jurka, J.; Rodriguez-Tome,
Claverie, J.M.; Dausset, J.; Cohen, D.
                                                                                                                                                                                                                                                                                                                                                            Conservative
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ses EMBL:Z15025; NID:g29374; PID:g29375
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Pred. No. 5.31e-01;
31; Mismatches 37
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#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2374-2378
#title A gene pair from the human major histocompatibility complex
encodes large proline-rich proteins with multiple repeated
motifs and a single ubiquitin-like domain.
#cross-references.MUID:90192810
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                                                                                                                                               1069 P-ARHGARVQSMRKSPSGAGSGAQKQAARPMRVIWLLQTRRLPHP 1112
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                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
##residues 1-2142 ##label BAN
##coss-references GB:M33509; NID:g179338; PID:g179339; GB:M31293
##note the authors translated the codon AGT for residue '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##note
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in the authors' translation residues 32-34 are shown
after residue 4 and, consequently, residues 5-31 are
displaced three codons to the right
the authors translated the codon AAT for residue 1000 as
His
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                                                                                                                           PVARLPAPAKPEQDSDSDSEGAAEGPAGAPRTLVRR-RRRRLLDP
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                                                                                                                                                                                                                                                                                       h 4.0%;
Similarity 29.5%;
31; Conservative
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Similarity 29.5%;
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MHC class III histocompatibility antigen HLA-B-associated
transcript 2 - human
#formal_name Homo sapiens #common_name man
10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change
10-Sep-1997
P1600
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Dense Alu clustering and a potential new member of the NFkappaB family within a 90 kilobase HLA class III segment. $336152
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I51734 #type complete
transcription factor isl-2 - zebra fish
insulin enhancer-binding protein isl-2;
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                                                                                                                                                                                                                                                                                                                                                                         #length 2142 #molecular-weight 227840 #checksum 5704
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Pred. No. 8.63e-01;
30; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 115; DB 2; Length 1872; Pred. No. 5.31e-01; 31; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                Length 2142;
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  islet-2 protein
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Best Local S
Matches 2
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89-142
192-248
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#title
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                                                                                                  melanogaster #cross-references MUID:90339481 #accession S11034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 PVRQPPHRNHVHKQSEKTTRVRTVLNEKQLHTLRTCYNANPRPD-ALM-KE-QLVEMTG- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary **molecule_type mRNA *#residue"
                                                           ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 LSPRVIRVWFQNKRCK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-359 ##label A1 ##cross-references EMBL:X88805;
                                          ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 VLPQSSRLFTLKIRCR 265
                     ##cross-references EMBL:X69965;
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Similarity 30.3%;
23; Conservative
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submitted to the EMBL Data Library, June 195
Motoneuron fate specification and patterned
expression in embryonic zebrafish.
S57407
                                                                                                                                                                                                                                                                               #type complete
gene Pl protein - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
21-Nov-1993 #sequence_revision 01-Dec-1995 #text_chance 24-Sep-1998
                                                                                                                                                           Lepesant, J.A.
J. Mol. Biol. (1990) 214:359-372
Structure of the ecdysone-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily transcription factor isl-1; homeobox homology;
LIM metal-binding repeat homology
DNA binding; duplication; homeobox; nucleus; transcription
regulation; zinc
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Molecular heterogeneity among primary motoneurons and within myotomes revealed by the differential mRNA expression of novel islet-1 homologs in embryonic rebrafish.
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#domain LIM metal-binding repeat homology #label
#domain homeobox homology #label HOX
#label HOX
#length 359 #molecular-weight 40227 #checksum 7994
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Tokumoto, M.; Gong, Z.; L.
Hotta, Y.; Okamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Brachydanio rerio #common_name zebra fish
13_Mar-1997 #sequence_revision 13-Mar-1997 #text_change
                                                                                                                                                                                                                              Maschat, F.; Dubertret, M.L.; Therond,
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                                                                                   preliminary
                                          1-1030 ##label
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Pred. No. 1.40e+00;
23; Mismatches 24; Indels
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                     NID:g7960; PID:g7961
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Claverie, J.M.;

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Best Local Similarity 31.6%;
Matches 18; Conservative
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Best Local Similarity 20.9%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal ViroLogy (1992) 186:280-285
#title The sequence of the genome of adenovirus type
#cross-references MUID:92087470
##moleon-1-
                                   #journal #title
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                                                                    #authors
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##cross-references GB:M73260
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##cross-references FlyBase:FBgn0000639
trons 31/1
# #length 1030 #molecular-weight 119364 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 DCVVLASSSEATE-TSQELRL 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 --LP-V-RMSEPLQNVVDHMANHLGVSPNRILLLFG-ESE-LSPTATPSTL-KLGVADII
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                                                                                                                                                                     #55973 #type fragment
transcription factor isl-2b - chinook salmon (fragment)
insulin enhancer-binding protein isl-2b; islet-2b prote
#formal_name Oncorhynchus tschawytscha #common_name chi
             Gong, Z.; Hui, C.; Hew, C.L.
J. Biol. Chem. (1995) 270:3335-3345
Presence of isl-1-related LIM domain homeobox genes
teleost and their similar patterns of expression 1
                                                                                                      B55973; S52091; S19956
                                                                                                                                       03-Oct-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                               #length 229 #molecular-weight 25164 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily adenovirus late 33K protein
late protein
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                                                                                                                        05-Sep-1997
spinal cord
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Pred. No. 2.84e+00;
14; Mismatches 24
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Pred. No. 1.40e+00;
66; Mismatches 76
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##molecule_type mRNA

##residues 1-340 ##label GON

##cross-references EMBL:X64884; NID:g64208; PID:g64209

##cross-references EMBL:X64884; NID:g64208 PID:g64209

##note authors translated the codon CTG for re

##note and ATG for residue 256 as Leu
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Best Local Similarity 28.9%;
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#journal Blochims. Blophys. Acta (1995) 1260:349-354
#title Several splicing variants of isl-1 like genes in the chine
salmon (Oncorhynchus tschawytscha) encode truncated
transcription factors containing a complete LIM domain.
#cross-references MUID:95178560
#accession $52091
                                       #map_position #introns
                      #note
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the authors translated the codon CAG for residue 105
##note His, GTG for residue 107 as Leu, CTG for residue 21
as Met, and ATG for residue 256 as Leu
                                                                                                                         ##residues 1-380 ##label ROU ##cross-references EMBL:AC003974; NID:g2914688;
                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 LVEMTG-LSPRVIRVWFQNKRCK 226
                                                                                                                                                                                              ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 VVLVEGPVLPQSSRLFTLKIRCR 265
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#residues 1-340 ##label GO2
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                                                                                                      ##experimental_source cultivar Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FHIADPVSVRQPPHRNHVHKQSEKTTRVRTVLNEKQLHTLRTCYNANPRPD-ALM-KE-Q
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hypothetical protein F24L7.10 - Arabidopsis thaliana
#formai_name Arabidopsis thaliana #common_name mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain LIM metal-binding repeat homology
#domain LIM metal-binding repeat homology
#domain homeobox homology #label HOX
#length 340 #checksum 5243
#length 380
                   55/3; 116/1; 161/3; 237/3; 287/3; 357/3
F24L7.10
                                                                                                                                                                                                            T00792
                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, February 1998 Arabidopsis thaliana chromosome II BAC F24L7 geno
                                                                                                                                                                                                                                                                                                               Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Ven
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LIM metal-binding repeat homology

DNA binding; duplication; homeobox; nucle
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  #molecular-weight 42844
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24; Mismatches 29
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Somerville, C.R.; Venter,
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Query Match
Best Local Similarity 25.6%; Pred. No. 2.24e+00;
Matches 20; Conservative 21; Mismatches 36; Indels 1; Gaps 1

Db 289 SRSPETSPHMKVTLKVKNQQGAEDLYKIGTHAHLKKLMSAYCTKRNLDYSSVRFVYNGRE 348

| : | | : | : : : | | | | |

Oy 332 SEATETSQELRLRYGKEKHOMLEI-SLSPDSPLKVLMSHYEEAMGLSGHKLSFFFDGTK 390

Db 349 IKARGYADLHLRYGKEKHOMLEI-SLSPDSPLKVLMSHYEEAMGLSGHKLSFFFDGTK 390

Oy 391 LSGKELPADLGLESGDLI 408

Search completed: Fri Feb 18 11:58:20 2000

Search completed: Fri Feb 18 11:58:20 2000
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************** (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

un on: bular output not generated. Fri Feb 18 11:58:36 2000; MasPar time 13.08 Seconds 890.539 Million cell updates/sec

Title: Description: Perfect Score:

Sequence: >US-08-755-584-2 (1-412) from 5858711.pep 2858 1 MAEPLRGRGPRSRGGRGARR.....GKELPADLGLESGDLIEVWG 412

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 50.879; Variance 107.959; scale 0.471

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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161 160 140 141 141 125 125 125 125 127 127 127 127 127 127 127 127 127 127	Score
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12 TENNDHINLKVAGQDGS-VVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPINET 70

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5.6% arity 32.9% Conservative	X99585; E274602; - 1089439; G1888536; 503042; - 108718; PS50053; UBIQUI NCE 95 AA; 10871	SWISS-PROT entry is copyright. It is produced through a collaineen the Swiss Institute of Bioinformatics and the EMBL outs European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in fied and this statement is not removed. Usage by and for couties requires a license agreement (See http://www.isb-sib.ch/aend an email to license@isb-sib.ch/.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SPECIES-BOVINE; TISSUE-ENDOMETRIUM; QI F., BERRY E.S.; SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA SUBFAMILY.	SEQUENCE FROM N.A. SPECIES-HUMAN; TISSUE-BRAIN; SPECIES-HUMAN; TISSUE-BRAIN; MEDLINE; 97237059. LAPENTA V., CHIURAZZI P., VAN DE! HANAOKA F., BRAHE C.; "SWT3A, a human homologue of the Chromosome 21qter and defines a i GENOMICS 40:362-367(1997).	T 1 SM32_HUMAN STANDARD; PRT; 95 AA. SM32_HUMAN STANDARD; PRT; 95 AA. 95865; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) UBIQUITIN-LIKE PROTEIN SMT3B (SEUTRIN 2). SMT3H2 OR SMT3B. SMT3
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
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01-NOV-1997 (REL. 35, LAST 9
15-JUL-1998 (REL. 36, LAST 7
UBIQUITIN-LIKE PROTEIN SMT3
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HANAOKA F.,
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01-NOV-1997
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GENOMICS 40:362-367(1997).
-i- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.
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HANAOKA F., BRAHE C.;
"SMT3A, a human homologue of the S.
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                                                                                                                                                                                                               "CHOUDHURY B.K., LI S.S.;
"Identification and characterization of the SMT3 cDNA and generatode Caenorhabditis elegans.";
BIOCHEM. BIOPHYS. RES. COMMUN. 234:788-791(1997).
-i- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "SMT3A, a human homologue of the S. cerevisiae SMT3 gene, ma chromosome 21qter and defines a novel gene family."; GENOMICS 40:362-367(1997).
-I- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.
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PROSITE; PS50053; UBIQUITIN_2;
DOMAIN 16 93 UI
                                        PROSITE; PS50053; UBIQUITIN_2;
                                                        EMBL; X99600; E259960; -
EMBL; U94830; G2341095;
                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                       GENOMICS 40
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*SMT3A, a human homologue of the S. cerevisiae SMT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAENORHABDITIS ELEGANS
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               SEQUENCE
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40:362-367(1997).
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               91
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35, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDAT
               10222 MW;
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25.7%;
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Pred. No. 1.14e-07;
26; Mismatches 28
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; CD7D6439 CRC32;
               UBIQUITIN-LIKE. F8E538FD CRC32;
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CAENORHABDITIS

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Best Local
Matches
                                                                                                                                                                                                                        MEDLINE; 96411684.
SHEN Z., PARDINGTON-PURTYMUN P.
CHEN D.J.;
"UBLL, a human ubiquitin-like p
RAD51/RAD52 proteins.";
GENOMICS 36:271-279(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM33_HUMAN STANDARD; PRT; 101 AA. Q93068; P55856; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) UBLOUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-RELATED (GAP MODLTYING PROTEIN 1) (GMP1) (SENTRIN).
                                                                                                                         "A small ubiquitin-related polypeptide involved in target to nuclear pore complex protein RanBP2."; CELL 88:97-107(1997).
                               nuclear
J. CELL
                                                                                                                                                                                                                                                                                                                                       BODDY M.N., HOWE K., ETKIN L.D., SOLOMON E., FREEMONT P.S.; "PIC 1, a novel ubiquitin-like protein which interacts with component of a multiprotein complex that is disrupted in accompelocytic leukaemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  HANAOKA F., BRAHE C.; "SMT3A, a human homologue of the S. cerevisiae SMT3 gene, chromosome 21qter and defines a novel gene family."; GENOMICS 40:362-367(1997).
SPECIES-HUMAN;
                                             the Ran-GTPase-activating nuclear pore complex.";
                                                                                                             SEQUENCE FROM N.A.
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MEDLINE; 97237059
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                                                                            MATUNIS
                                                                                                    SPECIES=HUMAN;
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                                                                MATUNIS M.J., COUTAVAS I
"A novel ubiquitin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391
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96400311.
                                                                                      97133418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.3%;
larity 22.5%;
Conservative
                              complex.";
. 135:1457-1470(1996)
           N.A
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 TISSUE-PLACENTA
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                                                              g., BLOBEL G.;
modification modulates the
                                                     protein RanGAP1
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31; M
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d. No. 1.55e-06;
Mismatches 30;
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SM31_HUMAN STANDARD;
P58854;
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O1-NOV-1997 (REL. 35, LA
O1-NOV-1997 (REL. 36, LA
UBLQUITIN-LIKE PROTEIN SI
SMT3H1 OR SMT3A,
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHOR
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EMBL; U61397; G151864; -.
EMBL; U38784; G1574948; -.
EMBL; U77122; G1762973; -.
EMBL; U72722; G1703503; -.
EMBL; U83117; G1769602; -.
EMBL; AF033353; G2645737; -.
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"Protection against Fas/APO-1- and tumor cell death by a novel protein, sentrin.";
J. IMMUNOL. 157:4277-4281(1996).
                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The ubiquitin-homology g and human (UBL1) genes an GENOMICS 47:92-100(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=MOUSE; STRAIN=ICR; MEDLINE; 98126440.
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. MOL. BIOL. 280:275-286(1998).
-I- FUNCTION: ASSOCIATES WITH RAD51/RAD52. INVOLVED IN TARGE RANGARI TO THE NUCLEAR PORE COMPLEX PROTEIN RANBP2.
-I- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMO-1."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98126440.
HOWE K., WILLIAMSON J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               3D-STRUCTURE.
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pseudogenes.";
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23; 1
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Pred. No. 4.07e-06;
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EC25C1FE CRC32;
    VERTEBRATA;
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    MAMMALIA;
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    SUTHERIA;
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
EUKARYOTIC TRANSLATON INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA) (EIF-4G)
                                                                                                                                                                                                                                                          LAMPHEAR B.J., YAN R., YANG F., WATERS D., LIEBIG H.-D., KLUMP H., KUECHLER E., SKERN T., RHOADS R.E., "Mapping the cleavage site in protein synthesis initiation eIF-4 gamma of the 2A proteases from human Coxsackievirus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                          "Amino acid sequence eIF-4 gamma.";
                                                                                                                       YAN R., RYCHLIK W., ETCHISON D., RHOADS R.E.; "Amino acid sequence of the human protein synthesis initiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                     ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IF4G_RABIT P41110;
                                                                                            J. BIOL.
                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                    PARTIAL SEQUENCE.
                                                                                                                                                                                                                                       rhinovirus."
                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                 STRAIN-NEW ZEALAND WHITE;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EIF4G) (P220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X99584; E274634; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 21qter and defines a novel GENOMICS 40:362-367(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HANAOKA F., BRAHE C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIMATES; CATARRHINI; HOMINIDAE; HOMO [1]
                                                                                                                                                                                                                                                                                                                                                                                                        LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 SGKELPADLGLESGDLIEV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 NETDTPAQLRMEDEDTIDV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 24; Conser
                                                                                                                                                                                                                          BIOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 EGVKTENDHINLKVAGQDGS-VVQFKIKRHTSLSKLMKAYCERQGLSMRQIRFRFDGQPI 66
                                BIOL. CHEM. 267:23226-23231(1992).

FUNCTION: COMPONENT OF THE PROTEIN COMPLEX EIF-4, WHICH IS INVOLVED IN THE RECOGNITION OF THE MRNA CAP, ATP-DEPENDENT UNWINDING OF 5'-TERMINAL SECONDARY STRUCTURE AND RECRUITMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATETSQE-LRLRVQGKEKHQMLEISLSPDSPLKVLMSHYEEAMGLSGHKLSFFFDGTKL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602231;
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                    TO THE RIBOSOME.
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                                                                                                                                                                 93054654.
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ilarity 30.4%;
Conservative
                                                                                                                                                                                                                      268:19200-19203(1993).
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CONTAINS 1 RNA RECOGNITION MOTIF (RNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11654 MW;
                                                                                                                                                                                                                                                                                                                                                   AND SEQUENCE OF 479-500 WHITE; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the S. cerevisiae SMT3 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAN DER SPEK P.J., PIZZUTI A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 141; DB 1; Lo
Pred. No. 5.10e-05;
20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UBIQUITIN-LIKE.
; 6E303BC0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Best Local 9
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SEQUENCE
                                    EMBL;
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                 PROSITE;
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                                                                                                                                                                                                                                     PELLETIER M.F., DIGNARD D.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                             SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMT3_SCHPO
O13351;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           UBIQUITIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: THE C-TERMINAL REGION IS SIMILAR TO THE N-TERMINAL REGION OF WHEAT EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82.
                                                                                                                                                                                                                                                                                                                                                            SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 ALSSRGP-PRGGPGGELPRGAAGLGPRRSLQPRPPKGARKLIASVIMTEDIKLNKAEKAW
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                                    AF019235; G2444268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n 4.5%;
Similarity 20.8%;
46; Conservative
  PS50053; UBIQUITIN_2; 1
7 87 UBI
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262
602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 129; DB 1; Le
Pred. No. 1.98e-03;
62; Mismatches 103;
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POLY-GLU.
RNA-BINDING
RNA-BINDING
  UBIQUITIN-LIKE
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NW; 6B00C346 CRC32;
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(RNP1)
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Matches 1
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Q12306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U27233; G881372; -.
EMBL; U37057; G927779; -.
SGD; L0001938; SMT3.
PROSITE; PS50053; UBIQUITIN_2; 1.
DOMAIN 22 101 UBIQUITIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                       01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDAT
FRAGILE X MENTAL RETARDATION SYNDROME RELAT
                                                                                                                                                                                                                                                                                                                          FXR2_HUMAN P51116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: NOT KNOWN; SUPPRESSOR OF MIF2 MUTATIONS.
-!- SIMILARITY: TO UBIQUITIN. BELONGS TO THE SMT3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. DIETRICH F.S.;
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EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMT3 OR YDR510W OR D9719.15
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01-NOV-1997 (REL. 35, LAST SEQUENCE UP
15-JUL-1998 (REL. 36, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLKVLMSHYEEAMGLSGHKLSFFFDGTKLSGKELPADLGLESGDLIE
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Similarity 33.3%;
16; Conservative
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101 AA; 11597 MW;
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27.48;
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TO EMBL/GENBANK/DDBJ DATA BANKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 125; DB 1;
Pred. No. 6.43e-03;
11; Mismatches 21
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Pred. No. 4.80e-03;
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Best Local s
Matches 2
                             MEDLINE; 9327;
IRIS F.J.M., 1
PERROT V., JU
                                                                                                                                                                                                                                       01-FEB-1996
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                      BAT2_HUMAN
P48634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                  BANERJI J., SANDS J., STROMINGER J.L., SPIES T.;
"A gene pair from the human major histocompatibility complex encodes large proline-rich proteins with multiple repeated motifs and a single ubiquitin-like domain.";
PROC. NATL. ACAD. SCI. U.S.A. 87:2374-2378(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long or modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96080171.
ZHANG Y., O'CONNOR J.P., SIOMI M.C
NUSSBAUM R.L., DREYFUSS G.;
"The fragile X mental retardation
novel homologs FXR1 and FXR2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
TISSUE-BRAIN;
"Dense Alu clustering and a family within a 90 kilobase
                      COHEN D.
                                                               SEQUENCE OF 1-1860 FROM N.A.
                                                                                                                                       MEDLINE; 90192810.
                                                                                                                                                  TISSUE=T-CELL;
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                  PRIMATES;
                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                             LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                  PVDSEPGEPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                n 4.0%;
Similarity 32.4%;
23; Conservative
                                                   93272029
                                                                                                                                                                                  CATARRHINI;
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295
414
544
584
                                JURKA
                                                                                                                                                                                                                                       (REL. 33, CREATED)
(REL. 33, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
                               BOUGUELERET L., PRIEUR URKA J., RODRIGUEZ-TOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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74128 .
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                                                                                                                                                                                             CHORDATA;
                                                                                 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 113;
Pred. No. 1.
18; Mismatc
potential new member of the NF kappa HLA class III segment.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KH.
KH.
POLY-SER.
POLY-ARG.
POLY-ARG.
                                                                                                                                                                                             VERTEBRATA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Le
1.93e-01;
ches 26;
                               CATERINA
CLAVERIE
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                              D., PRI
J.-М.,
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                               PRIMAS G.,
M., DAUSSET
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NAT. GENET. 3:137-145(1993).
-!- FUNCTION: UNKNOWN.
-!- TISSUE SPECIFICITY: LIMI

SPECIFICITY: LIMITED TO CELL-LINES OF LEUKEMIC ORIGIN

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EMBL; M33518; G179345; -.
EMBL; M33512; G179345; JOINED.
EMBL; Z15025; G29375; -.
PIR; B35098; B35098.
PIR; S36152; S36152.
ISL2_BRARE
P53406;
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Similarity 29.5%;
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                                                Query Match
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Matches 2
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EMBL; U09403; G487805; -.
EMBL; X88805; G871001; -.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 2.
PROSITE; PS50071; HOMEOBOX_2; 1.
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01-0CT-1996 (REL. 34, I
01-0CT-1996 (REL. 34, I
INSULIN GENE ENHANCER F
ISL2 OR ISL-2.
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression in embryonic zebrafish.";
DEVELOPMENT 121:4117-4125(1995).
-I- FUNCTION: BINDS TO ONE OF THE CIS-ACTING DOMAIN OF THE INSULIN
GENE ENHANCER. MAY BE INVOLVED IN SUBTYPE SPECIALIZATION OF
                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00046; homeobox; 1. PFAM; PF00412; LIM; 2. HSSP; P02836; 1HDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular heterogeneity among primary motoneurons and within myotomes revealed by the differential mRNA expression of novel islet-1 homologs in embryonic zebrafish."; DEV. BIOL. 171:578-589(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OKAMOTO
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI: EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; RASBORINAE; DANIO.
                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Motoneuron fate specification revealed by gene expression in embryonic zebrafish.";
174 PVRQPPHRNHVHKQSEKTTRVRTVLNEKQLHTLRTCYNANPRPD-ALM-KE-QLVEMTG- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR.

DEVELOPMENTAL STACE: FIRST EXPRESSED AFTER 15 H OF GASTRULATION,
SEGMENTALLY IN THE VENTRAL REGION OF THE SPINAL CORD AND THEN
LATER IN THE DORSAL REGIONS (ROHAN-BEARD NEURONS).

SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2
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                                                   Similarity
23; Conser
                                                                                                                                                            LIM MOTIF; METAL-BINDING; ZINC; MULTIGENE FAMILY.

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GLN-RICH.
E 359 AA; 40227 MW; DC592CD0 CRC32;
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96125154.
, KORZH V.,
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                                                                                                                                                                                                                                                                                                                              DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
                                                3.9%;
llarity 30.3%;
Conservative
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LAST ANNOTATION UPDATE)
PROTEIN ISL-2 (ISLET-2)
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                                                Score 111;
Pred. No. 3.
23; Mismatc
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                                                      Mismatches
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                                                                               DB 1;
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p52157;
01-OCT-1996 (REL. 3
01-OCT-1996 (REL. 3
01-NOV-1997 (REL. 3
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SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (FEB-11996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: FACILITATES TRANSCRIPTION TERMINATION BY A MECHANISM
THAT INVOLVES RHO BINDING TO THE NASCENT RNA, ACTIVATION OF RH
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Q80903;
                                                                        STRAIN-ZX7;
INGHAM C.J.,
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15-JUL-1998
15-JUL-1998
                                                                                                                                                                     ACTINOMYCETALES;
                                                                                                                                                                                      STREPTOMYCES LIVIDANS. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                              FRANSCRIPTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%;
Similarity 44.7%;
21; Conservative
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8 (REL. 36, LAST)
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34, LAST SEQUENCE UPDATE)
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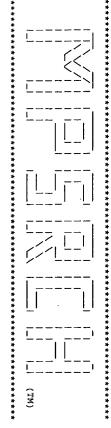
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"Deletion scanning of the regulatory sequences of the Fbpl gene (Drosophila melanogaster using P transposase-induced deficiencies. GENETICS 135:801-816(1993).
-!- TISSUE SPECIFICITY: FAT BODY.
                                                                                                                                                                                                         STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X95444; E220353; -.
EMBL; X95444; E220354; ALT_INIT.
HSSP; P03002; 1A62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                         MEDLINE; 90339481.
MASCHAT F., DUBERTRET M.-L., THEROND
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CANTON-S; TISSUE=FAT
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                                                                                                                                                                                                                                                                                      melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DROSOPHILA MELANOGASTER (FRUIT FLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
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SIMILARITY: CONTAINS 1 RNA RECOGNITION
CAUTION: IT IS UNCERTAIN WHETHER MET-1
              European Bioinformatics Institute.
                                                                               INDUCTION: BY ECDYSONE
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                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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DIPTERA;
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Best Local Similarity 20.9%;
Matches 42; Conservative
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EMBL; x69965; G7961; -.
PIR; S11034; S11034.
FIXBASE; FB90000639; Fbp1.
PFAM; PF00372; hemocyanin; 2.
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17 1030 FAT-BODY PROTEIN-1.
360 371 POLY-ASP.
580 590 POLY-ASP.
741 741 POTENTIAL.
1030 AA; 119365 MW; A3AC5F31 CRC32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. Fri Feb 18 11:59:45 2000; MasPar time 26.42 Seconds 850.987 Million cell updates/sec

Title: Description: Perfect Score: Sequence: >US-08-755-584-2 (1-412) from 5858711.pep 2858 1 MAEPLRGRGPRSRGGRGARR.....GKELPADLGLESGDLIEVWG 412

Scoring table: PAM 150 Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 48.921; Variance 112.296; scale 0.436

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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109 3.8 338 4 000365 LI ELEMENT L1.15 P40 A 108 3.8 38 4 000371 LI ELEMENT L1.121 P40 A 109 3.8 380 10 048841 F24L7.10 PROTEIN. 109 3.8 410 2 006224 MYELOBLAST KIRA0239 (F 108 3.8 1210 13 092137 PHOSPHOLIFASE C BETA T 110 3.8 1215 10 P93750 ULJ6. 110 3.8 1215 10 P93750 ULJ6. 110 3.8 3247 14 065553 ULJ6. 110 3.8 3247 14 065553 ULJ6. 110 3.7 116 14 070677 REV PROTEIN. 110 3.7 123 14 089930 ORF E PROTEIN. 110 3.7 123 14 089930 ORF E PROTEIN. 110 3.7 338 4 000364 LI ELEMENT L1.14 P40 A 110 3.7 338 4 000361 LI ELEMENT L1.39 P40 A 110 3.7 338 4 000361 LI ELEMENT L1.39 P40 A 110 3.7 338 4 000361 LI ELEMENT L1.39 P40 A 110 3.7 338 4 000361 LI ELEMENT L1.39 P40 A 110 3.7 338 4 000361 LI ELEMENT L1.39 P40 A 110 3.7 338 4 000361 LI ELEMENT L1.39 P40 A 110 3.7 310 042417 SERINE PROTEIN. 110 3.7 381 2 048919 FIBRONECTIN ATTACHMENT 110 3.7 310 042417 SERINE PROTEIN. 110 3.7 1066 5 026080 MYOSIN HEAVY CHAIN. 110 3.7 313 4 013246 NUCLEAR PHOSPHOPROTEIN 110 3.7 313 4 013246 NUCLEAR PHOSPHOPROTEIN	45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28	27	26	25	24	23	22	21
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	POLYPROTEIN.			HEAVY		(EC 3.2.1.	C49G7.1 PROTEIN.		SERINE PROTEASE (FRAGM		NITROGENASE MO-FE PROT	ELEMENT L1.39 P40	L1.8 P40	ELEMENT L1.14 P4	Ħ			UL36.		C BETA	KIAA0239 (MURG.	F24L7.10 PROTEIN.	ELEMENT L1.21	ELEMENT L1.15

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                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. CASTELLANA; TISSUE-ETIOLATED MUNCZ F.J., DOPICO B., LABRADOR E.;
PLANT PHYSIOL. 116.1605-1605(1998).
EMBL; AJ001901; E354254; -.
SEQUENCE 115 AA; 12858 MW; 89C22D7C
                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAU-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
UBIQUITIN PROTEIN.
                                                                                                                                                                                                                                                     CICER ARIETINUM (CHICKPEA) (GARBANZO).
EUKARYOTA; VIRIDIPLANYAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MGNOLLOPHYTA; EUDICOTYLEDONS; ROSI
FABALES; FABACEAE; PAPILIONOIDEAE; CICER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Ubc9p and the conjugation of CURR. BIOL. 8:121-124(1998).
EMBL; 297073; E323533; -
SEQUENCE 102 AA; 11703 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAITOH H., SPARROW D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMO-1 PROTEIN.
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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    394 KELPADLGLESGDLIE 409
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                              76
                                                                    18 PNDAAH-INLKVKGQDGNEVF-FRIKRNTQLKKLMNAYCDRQSVDLNSIAFLFDGRRLRA 75
                                                                                                         / Match 5.6%;
Local Similarity 25.0%;
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 GDKKDGGDYIKLKVIGQDSSEI-HFKVKMTTHLKKLKESYRQRQGVPMNSLRFLFEGQRI 72
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                              EQTPDELDMEDGDEID
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21; Conser
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llarity 26.6%;
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                                                                                                                                                            12858 MW; 89C22D7C CRC32;
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Pred. No. 4.
27; Mismatc
                                                                                                         Score 161; DB 10;
Pred. No. 4.33e-07;
30; Mismatches 25;
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1.33e-07;
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Best Local :
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074186;
01-NOV-1998
01-NOV-1998
01-NOV-1998
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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
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SEQUENCE
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057114;
057114;
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
NONSTRUCTURAL PROTEIN P125-2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                "The fission yeast ubiquitin-like modifier."; SUBMITTED (AUG-1998) TO EMBL/GENBARK/DDBJ DATA BANKS. EMBL; ABOJ7187; D1033560; -. SEQUENCE 117 AA; 12934 MW; 9807EC2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (FEB-1997) TO EMBL; U89438; G2707597; NONSTRUCTURAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PESTIVIRUS TYPE 1.
VIRUSES; SSRNA POSITIVE-STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
NISHIDE J., NISHI T., MURAKAMI Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMT3P.
                                                                                                                                                                                                                                                                                                                                                                                                        TANAKA K.;
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                                                 83
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                                                                                                                                                 24 TSQQDVKPSTEHINLKYVGQDNNEVF-FKIKKTTEFSKLMKIYCARQGKSMNSLRFLVDG 82
                            ERIRPDQTPAELDMEDGDQIE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TETSQELRLRVQGKEKHQMLEISLSPDSPLKVLMSHYEEAMGLSGHKLSFFFDGTKLSGK 394
  TKLSGKELPADLGLESGDLIE
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Similarity 32.9%;
25; Conservative
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21; Conser
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239 AA;
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                                                                                                                                                                                                4.6%;
|llarity 25.9%;
| Conservative
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26881 MW;
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     409
                                                                                                                                                                                                   Score 131; DB 3;
Pred. No. 3.41e-03;
24; Mismatches 35
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 4.33e-07;
19; Mismatches 31
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RESULT 6

PRELIMINARY;

PRT;

1173 AA

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Matches 3
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STRAIN-21068;
LOLE K.S., BOLLINGER R.C., PARANJAPE R.S., GADKARI D.,
NOVAK N.G., INCERSOLL R., SHEPPARD H.W., RAY S.C.;
"Molecular cloning and full-length sequencing of human
immunodeficiency virus type 1 genomes from subtype C-in
seroconverters in India, with evidence of inter-subtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q63624;
01-NOV-1996
01-NOV-1996
01-NOV-1998
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GEBARA M., CORDEN J.L.;
"The C-terminal domain of the largest subunit of RN interacts with a novel set of serine/arginine-rich PROC. NATL. ACAD. SCI. U.S.A. 93:6975-6980(1996).
EMBL; U49055; G1438532;
SEQUENCE 1173 AA; 124774 MW; B01EBCE2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
CTD-BINDING SR-LIKE PROTEIN RAI
RATTUS NORVEGICUS (RAT).
RATTUS NORVEGICUS (RAT).
                                                                                                                                                 SUBMITTED (MAY-1998)
EMBL; AF067155; G3252
SEQUENCE 107 AA; 1
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     VIRUSES;
                                                                                                                                                                                                                                                                                                               HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=HIPPOCAMPUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 96293459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
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                                                                        RGTRQARKNRRRRWRARQRQIHSISERILSTFLGRPAEPVPLQLP-PIE-RL-HISGSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRKILTQ-RR-ERYRQRSASPGP-PPARKKARRERQ 425
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 PEQDSDSDSEGAAEGPAGAP
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24; Conse
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larity 24.4%;
Conservative
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                                                                                                                                                                                                                                                                                                    VIRUSES;
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                                                                                                                                                                        TO EMBL/GENBANK/DDBJ DATA
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                                                                                                                                                                                                                                                                                                                                                    888
                                                                                                                                                 WW;
 94
                        107
                                                                                                                                                                                                                                                                                                    RETROVIRIDAE; LENTIVIRUS
                                                                                                Score 123;
Pred. No. 3.
28; Mismatc
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41; 1
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                              TYPE 1 (HIV-1)
                                                                                                                                                CB254F1F CRC32;
                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                           DB 14;
3.20e-02;
                                                                                                                                                                                                of inter-subtype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1173;
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Matches 3
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                                                                    043770; PRELIMINARY;
043770; (TREMBLREL, 0
01-JUN-1998 (TREMBLREL, 0
01-JUN-1998 (TREMBLREL, 0
01-JUN-1998 (TREMBLREL, 0
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006470;
01-JUL-1997
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01-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARRON R.L., BARRY J.J., SUBMITTED (APR-1997) TO E EMBL; U97042; G2109270; - SEQUENCE 405 AA; 44441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THESIS (1991), UNIVERSITY OF WISCO-1- CATALYTIC ACTIVITY: XYLITOL + EMBL; L34345; G508520; -. PFAM; PF00107; adh_zinc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MORGANELLA MORGANII (PROTEUS MORGANII)
BACTERIA; PROTEOBACTERIA; GAMMA SHRDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
XYLITOL DEHYDROGENASE (EC 1.1.1.9) (D-XYLULOSE REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-K61-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BURKHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA). BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEOA.
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Local Similarity 27.4%;
tes 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            VEVPVARLPAPAKPEQDSDSDSEG-AAEGPAGAPRTLVR
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34; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TREMBLREL.)
(TREMBLREL.)
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                                                                             888
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EMBL/GENBANK/DDBJ DATA
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23; N
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Pred. No. 9.52e-02;
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No. 9.52e-02
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PROTEIN.

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Best Local :
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NOMURA N., OHARA O.;
Characterization of cDNA clones in from human brain.";
DNA RES. 4:345-349(1997).
EMBL; AB007919; D1033257; -.
EMBL; AB007919; D1033257; -.
               SULT 12
O06359 PRELIMINARY; PRT; 7'
O06359; O1-JUL-1997 (TREMBLREL 04, CREATED)
O1-JUL-1997 (TREMBLREL 04, LAST SEQUE)
O1-NOV-1998 (TREMBLREL 08, LAST ANNOT.
HYDOTHETICAL 81.4 KD PROTEIN.
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075038;
01-NOV-1998
01-NOV-1998
01-NOV-1998
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KIAAUSJU.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUKARYOTA; MOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSBORNE L.R., JADAYEL D.M., COIGNET L.J., SCHEKER S.W., DYER M.J.; SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ EMBL; AJ223980; E1249849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
HOMO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                    RIPAPAKPEQDSDSDSEGAAEGPAG-APRTLVRRRRRLLD-PGEAPVVP
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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8 (TREMBLREL.
9 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                              4.18;
larity 31.58;
Conservative
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larity 26.18;
Conservative
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LAST SEQUENCE ANNOTED
                                                                                                                                                                                                                                                                                                                                                                                            Score 117; DB 4;
Pred. No. 1.63e-01
25; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISHIKAWA K., MIYAJIMA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                               UPDATE)
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                                                                                                                              Query Match
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Best Local 9
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Q69511;
Q1-NOV-1996
Q1-NOV-1996
Q1-AUG-1998
                                                                                                                                                                                                                                                        NICHOLAS J.;
SUBMITTED (DEC-1995) TO EMI
EMBL; U43400; G1139682; -.
NON_TER 1 1
SEQUENCE 210 AA; 23935 )
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BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRUSES; DSDNA VII
BETAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-J
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Mycobacterium tuberculosis H37Rv,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN HERPESVIRUS TYPE
VIRUSES; DSDNA VIRUSES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HERPESVIRUS-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLE S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHILIPP W.J., POULET S., BALASUBRAMANIAN V., HEYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96181548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378
                                                                     149
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eprae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 4.18;
Local Similarity 24.68;
      ø
STRSRGRSRGRPRGRG-RSRNMSMRQTP-REVEDMLPIVLDSDSDTETL
: |||| :|| ||:| ||:| | : | |||| || ||
GPRSRG-GRGARRARGARGRCPRARQSPARLIPDTVLVDLVSDSDEEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVVLASSSEATETSQELRLRVQGKEKHQMLEISLSPDSPLKVLMSHYEEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVNKRIQDIRSCISPKQHQSPALQSTDDEVVLVEGPVLPQSSRLFTL-KIRCRADLVRL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTVALWEPALRSDVIG-EHGAPVRRSAGAEAARVMADLIVEGAQTLTFVRSRRAAELTAL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVVLAGFPGTVASFWQQAGRS-GRRGQGALVVLIARDDPLDTYLVHHPAAL 427
                                                                                                                              h 4.0%;
Similarity 46.9%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARRELL B.
(MAY-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAY-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHURCHER C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
-7 (HHV7) JI, COMPLETE VIRION GENOME (FR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 X
                                                                                                                                                                                                                                                               23935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
6
7
                                                                                                                                                                                                                                                                                                                                                            TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAJANDREAM M.A.;
EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIGLMEIER
B., BERGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLETE VIRION GENOME (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 117; DB 2;
Pred. No. 1.63e-01;
47; Mismatches 72
                                                                                                                              Score 114; DB 14;
Pred. No. 3.61e-01
8; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93:3132-3137(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                               EC2EEDD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48B7AFB6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ς; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ne tubercle bacillus, comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PASCOPELLA :
BLOOM B.R.,
                                                                                                                                                                                                                                                               CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATA
                                                                                                                                                                                                                                                                                                                                                               DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BANKS
                                                                                                                                                                                             Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , JACOBS
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYCOBACTERIUM
         56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                    w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTEN N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTEN B., O'CALLAGHAN M.,
LIGHTNING J., LLOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M. Of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                    056296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q20393;
Q20393;
STRAIN-RK;
MEGAW A.G., FRENKEL N., DAVISON A.J.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF037218; G2746308; -.
                                                                                           MEDALINE; 98240941
MEGAW A.G., RAPAPORT D., AVIDOR B.,
"The DNA sequence of the RK strain c
VIROLOGY 244:119-132(1998).
                                                                                                                                                                                                                                                         01-JUN-1998 (TREMBLREL 06, CREATED)
01-JUN-1998 (TREMBLREL 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 58.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL 01, 01-NOV-1996 (TREMBLREL 01, 01-JAN-1999 (TREMBLREL 09,
                                                               SEQUENCE FROM N.A.
                                                                                                                                                      STRAIN-RK;
                                                                                                                                                                                                   BETAHERPESVIRINAE
                                                                                                                                                                                                               HUMAN HERPESVIRUS 7.
VIRUSES; DSDNA VIRUSES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATURE 368:32-38(1994).
EMBL; Z68298; E1346770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHABDITINA; RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F44D12.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                              65 PVARL 69
                                                                                                                                                                                                                                                                                                                                                                                                                          59 AAKEL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ر.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRGRGPRSRGGRGARRARGARGRCPRARQSPARLIPDTVLVDLVSDSDEEVLEVADPVEV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%;
larity 29.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                 RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 5; L
Pred. No. 4.69e-01;
19; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                              STAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2EA853D3 CRC32;
                                                                                                         of human herpesvirus 7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352
                                                                                                                                                                                                                                                                                                                                   506 AA.
                                                                                                                                                                                                                 HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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KW HYPOTHETICAL PROTEIN.

SQ SEQUENCE 506 AA; 58462 MW; 967FD02B CRC32;

Query Match

4.0%; Score 114; DB 14; Length 506;

Best Local Similarity 46.9%; Pred. No. 3.61e-01;

Matches 23; Conservative 8; Mismatches 15; Indels 3; Gaps
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Search completed: Fri Feb 18 12:01:45 2000 Job time : 120 secs.

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